



Docket No.: CL001187

Serial No.: 09/817,199

Inventors: SHAO, Wei et al.

Title: ISOLATED HUMAN RAS-LIKE PROTEINS...

```
1 TTCGCCTGCG GGCCGGCACT GCTCACCTCT CGTCCAGGGA CATGACGGGC
51 ACGCCAGGCG CCGTTGCCAC CCGGGATGGC GAGGCCCCCG AGCGTCCCC
101 GCCCTGCACT CCGAGCTACG ACCTCACGGG CAAGGTGATG CTTCTGGGAG
151 ACACAGGCGT CGGCAAAACA TGTTTCCTGA TCCAAATCAA AGACGGGGCC
201 TTCCTGTCCG GAACCTTCAT AGCCACCGTC GGCATAGACT TCAGGAACAA
251 GGTGGTGACT GTGGATGGCG TGAGAGTGAA GCTGCAGATC TGGGACACCG
301 CTGGGCAGGA ACGGTTCCGA AGCGTCACCC ATGCTTATTA CAGAGATGCT
351 CAGGCCTTGC TTCTGCTGTA TGACATCACC AACAAATCTT CTTTCGACAA
401 CATCAGGGCC TGGCTCACTG AGATTTCATGA GTATGCCAG AGGGACGTGG
451 TGATCATGCT GCTAGGCAAC AAGGCGGATA TGAGCAGCGA AAGAGTGATC
501 CGTTCCGAAG ACGGAGAGAC CTTGGCCAGG GAGTACGGTG TTCCCTTCCT
551 GGAGACCAGC GCCAAGACTG GCATGAATGT GGAGTTAGCC TTTCTGGCCA
601 TCGCCAAGGA ACTGAAATAC CGGGCCGGGC ATCAGGCGGA TGAGCCAGC
651 TTCCGATATC GAGACTATGT AGAGTCCCAG AAGAAGCGCT CCAGCTGCTG
701 CTCCTTTCATG TGAATCCAG GGGGCAGAGA GGAGGCTCTG GAGGCACACA
751 GGATGCAGCC TTCCCCCTCC CAGGCCTGGC TTATTCCAAG AGGCTGAGCC
801 AATGGGGAGA AAGATGGAGG ACTCACTGCA CAGCCGCTTC CTAGCAGGGA
851 GCTATACTCC AACTCCTACT TGAGTTCCTG CGGTCTCCCC GCATCCACAG
901 GGAGGGTAAA ACACCTTAGCT TTTATTTTAA TAGTACATAA TTTAATAACA
951 AAAAAGGCGC CTGGATCCCC AAAAAACCGA GGCTGGGAGC TAGTGGCCCT
1001 TTTGGTTTCT AGGAGTTGGG GGGGGGGGEC TCCGTCGTAA GEATAAGAAA
1051 GGTGGTGTTG CTCCAGCTCA GCCCCAGGGG ACACAGATGC ACTTTGGGGG
1101 TGAGGGCAGG TAATGACTCC ATCGCACCCCT CAGTTCAGCT GGACAGAGGC
1151 TCAGGTGACC CCAGCCTTCA CTGTCTCCCG CTCTCCAGGA GCTTATCTTC
1201 GCCCCATCTC CCAAATAAGT GGGCCCTTGT GCTGTGAGGA AGACCAAAGC
1251 CTCAGGGAAG ATAAGAGATA TGGAGATGGG AGGGGGAGGA CAAGGGGCAG
1301 AGAGTAGGGT CTAGCTGGCT ATCTCTGGCC TTAATAACAC CCCCCTGGAG
1351 GCATGCCCCCT TTTCTCCAGC ACACAAGCAC ATTGGGGCAC CTGGAATAT
1401 TGGTTCCAGG CTCCTGTTCT CTGGACTTCA GATCCTGGGG GAGCCCCCTCC
1451 CCCCCCTGAA TCCCTGGCTT AGCTACCTTC CTGCCTGTGC ACCTAAAAAC
1501 CTCAGGTGAG AACTAGGAAA AGAGTTTGT TTTTATTTT TTGAAATGGA
1551 GTCTCGTTCT GTCGCCCAGG CTGAGGTGCA GTAGTGCAAT CTCCGCTCAC
1601 TACAACCTCC ACTCCCTGGG GCTCAAGCGA TCCTCCACC TCAGCCGCG
1651 AAGTAGCTGG GACTATAGGT GTGTACCATC ACACCTGGCT AATTTTGTGA
1701 TTTTTTGTAG ACACAGGTT TCGCCATGTT GCCCAGGCTG GTCTTGAATT
1751 CCTGAGCTCA AGCAACCTGC CGGCCTCGGC CTCCCAAAGT ACTGGGATTA
1801 CACGCAGAAG GCACCATGCC CAGGCTAGAT GTGTCTTATC CCAATCCTTT
1851 GGCAGGCATG CAGCTCCACA GGCGATTCT TCAAGCAGCT GAAGTGTTTA
1901 GCCCTCCTGG GTTAAGAGCC AGATAAGGAG AAATCCCTTT CTTAGGTTTG
1951 GAATGTGTTG TGAAAAAAA GAGAAATCCC TGGCTCCTGT AGCTGGTGGG
2001 AGACAAGATT AAGCAAAACCT CCCCTGACAT GTATCCCTTT GACCCCAAGC
2051 TCTGCCTCCT CCCTGACCAC CCATGCCCTT TCCTTTAACT TCTCAAACAG
2101 ATACCAGGGC CTAAACTGCT TTACCTCCCC TCCTACTGAG TCAGGTTAGG
2151 TGGTGGGAGG TCACCCATTT CCGAGTTAAA CCAATGCAAT ATGAGTAAAA
2201 CAAAGTCATG TGGGTATGTC TGGGGTAGAG AGAGGGGTAG CAAGTTCATG
2251 TGTCTCCTT GGTACATAT CTCCCAAAGC TCTGATCCCT GCCATGGGAA
2301 GTGGACAGGA AACATGAGGT CATGACCTGC AGGCATCTTT ACTGCAGCTC
2351 TGCCGGCCTG GAGGGGGAGA GGGGGAGGAA GAAGTATGCG CTGCACATTT
2401 CTGAGGCTAC TGCATTGCT TTCAAGGCAG AAATCTTGCT CTGAGCAGTC
2451 AGCGGCTCCA GTTTGGGCCC GATAAGGAAG TTCTCCGTGG CCTCCCTCAG
2501 GCAGAGCAGG GAGGAGGCTG ACATTGCCAG TCTCTTCTGG GGCCCAAGGC
2551 AGGTTGCAGG AGATCCAATC CCATAGACAG CTCTGGGCCT CTTGCATTTG
2601 AGTTTTTCAG AATTAACTG CAGTATTTTG GAAAGCAAAA AAAAAAAAAA
2651 AAAAAAAAAA AAAAAAAAAA AAAA (SEQ ID NO:1)
```

FEATURES:

5'UTR: 1-41
Start Codon: 42
Stop Codon: 711
3'UTR: 714

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FIGURE 1A



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Homologous proteins:

Top 10 BLAST Hits

	Score	E
CRA 103000001517087 /altid=gi 10946770 /def=ref NP_067386.1 RA...	425	e-117
CRA 1000682330460 /altid=gi 7657492 /def=ref NP_055168.1 RAB26...	297	4e-79
CRA 18000004977238 /altid=gi 1710022 /def=sp P51156 RB26_RAT RA...	294	3e-78
CRA 18000005013109 /altid=gi 1083775 /def=pir JC2528 GTP-bindi...	293	7e-78
CRA 89000000198627 /altid=gi 7296421 /def=gb AAF51708.1 (AE003...	273	9e-72
CRA 18000005076419 /altid=gi 7438397 /def=pir T15123 hypotheti...	207	4e-52
CRA 18000004912300 /altid=gi 134236 /def=sp P20791 SAS2_DICDI G...	203	7e-51
CRA 98000043536338 /altid=gi 12963499 /def=ref NP_075615.1 cel...	203	9e-51
CRA 18000004929618 /altid=gi 131798 /def=sp P24407 RAB8_HUMAN R...	202	1e-50
CRA 18000004952869 /altid=gi 131848 /def=sp P22128 RAB8_DISOM R...	202	2e-50
CRA 18000005221564 /altid=gi 4586580 /def=dbj BAA76422.1 (AB02...	202	2e-50

BLAST dbEST hits:

	Score	E
gi 13033710 /dataset=dbest /taxon=960...	1318	0.0
gi 12785775 /dataset=dbest /taxon=960...	1316	0.0
gi 12904236 /dataset=dbest /taxon=960...	1035	0.0
gi 9093496 /dataset=dbest /taxon=9606...	694	0.0

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

From BLAST dbEST hits:

gi|13033710 prostate
gi|12785775 brain
gi|12904236 T cells from T cell leukemia
gi|9093496 leukopheresis

From tissue screening panels:

leukocyte

FIGURE 1B



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1 MTGTPGAVAT RDGEAPERSP PCSPSYDLTG KVMLLGDGTG GKTCFLIQFK
51 DGAFLSGTFI ATVGIDFRNK VVTVDGVRVK LQIWDTAGQE RFRSVTHAYY
101 RDAQALLLLY DITNKSSFDN IRAWLTEIHE YAQRDVVIML LGNKADMSSE
151 RVIRSEDGET LAREYGV PFL ETSAKTGMNV ELAFLAIAKE LKYRAGHQAD
201 EPSFQIRDYV ESQKKRSSCC SFM (SEQ ID NO:2)

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FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

114-117 NKSS (SEQ ID NO:5)

[2] PDOC00004 PS00004 CAMP_PHOSPHO_SITE
cAMP- and cGMP-dependent protein kinase phosphorylation site

Number of matches: 2

1 214-217 KKRS (SEQ ID NO:6)
2 215-218 KRSS (SEQ ID NO:7)

[3] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 5

1 29-31 TKG
2 113-115 TNK
3 149-151 SER
4 173-175 SAK
5 212-214 SQK

[4] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

116-119 SSFD (SEQ ID NO:8)

[5] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 5

1 3-8 GTPGAV (SEQ ID NO:9)
2 6-11 GAVATR (SEQ ID NO:10)
3 39-44 GVGKTC (SEQ ID NO:11)
4 52-57 GAFLSG (SEQ ID NO:12)
5 57-62 GTFIAT (SEQ ID NO:13)

[6] PDOC00017 PS00017 ATP_GTP_A
ATP/GTP-binding site motif A (P-loop)

36-43 GDTGVGKT (SEQ ID NO:14)

[7] PDOC00579 PS00675 SIGMA54_INTERACT_1
Sigma-54 interaction domain ATP-binding region A signature

32-45 VMLLGDGTGVGKTCF (SEQ ID NO:15)

Membrane spanning structure and domains:

Helix Begin	End	Score	Certainty
1 48	68	0.715	Putative

FIGURE 2A



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BLAST Alignment to Top Hit:

>CRA|103000001517087 /altid=gi|10946770 /def=ref|NP_067386.1| RAB37,
member of RAS oncogene family; GTPase Rab37 [Mus
musculus] /org=Mus musculus /taxon=10090 /dataset=nraa
/length=223
Length = 223

Score = 425 bits (1081), Expect = e-117
Identities = 209/223 (93%), Positives = 215/223 (95%)
Frame = +3

Query: 42 MTGTPGAVATRDGEAPERSPPCSPSYDLTGKVMLLGDTGVGKTCFLIQFKDGAFLSGTFI 221
MTGTPGA DGEAPERSPP SP+YDLTGKVMLLGD+GVGKTCFLIQFKDGAFLSGTFI
Sbjct: 1 MTGTPGAATAGDGEAPERSPPFPSNYDLTGKVMLLGDSGVGKTCFLIQFKDGAFLSGTFI 60

Query: 222 ATVGIDFRNKVVTVDGVRVKLQIWDTAGQERFRSVTHAYYRDAQALLLLYDITNKSSFDN 401
ATVGIDFRNKVVTVDG RVKLQIWDTAGQERFRSVTHAYYRDAQALLLLYDITN+SSFDN
Sbjct: 61 ATVGIDFRNKVVTVDGARVKLQIWDTAGQERFRSVTHAYYRDAQALLLLYDITNQSSFDN 120

Query: 402 IRAWLTEIHEYAQRDVVIMLLGNKADMSSERVIRSEDGETLAREYGVFPFLETSAKTGMNV 581
IRAWLTEIHEYAQRDVVIMLLGNKAD+SSERVIRSEDGETLAREYGVFP+ETSAKTGMNV
Sbjct: 121 IRAWLTEIHEYAQRDVVIMLLGNKADVSSERVIRSEDGETLAREYGVPFMETSAKTGMNV 180

Query: 582 ELAFLAIAKELKYRAGHQADEPSFQIRDYVESQKKRSSCCSF 710 (SEQ ID NO:2)
ELAFLAIAKELKYRAG Q DEPSFQIRDYVESQKKRSSCCSF+
Sbjct: 181 ELAFLAIAKELKYRAGRQPDEPSFQIRDYVESQKKRSSCCSFV 223 (SEQ ID NO:4)

Hammer search results (Pfam):

Model	Description	Score	E-value	N
PF00071	Ras family	306.9	8.4e-90	1
CE00060	CE00060 rab_ras_like	213.3	3.7e-60	1
PF01142	Uncharacterized protein family UPF0024	2.6	3.4	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
CE00060	1/1	31	191 ..	25	193 ..	213.3	3.7e-60
PF01142	1/1	185	201 ..	444	462 .]	2.6	3.4
PF00071	1/1	31	223 .]	1	198 []	306.9	8.4e-90

FIGURE 2B



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1 AGGGGAGAGA AAAGACCGCA TACCAGGCCA GGTGCGGTGG CTCACGCTTG
51 TAATCCCAGC AATTTTGAAG GCCAAGGCAG GCGTATCGCC TGAGGTCAGC
101 AGTTCCAAAC CAGCCTGTCC AACATGGTGA AGTTCTCTAC TAAGAATACA
151 AAAATTACCC AGGCGTGGTG GCGTGACCTT GTAGTCCCAG CTGCTCCAGA
201 GGCTGAGGCA GGAGAAATGC TTGAACCTGG GAGGCAGAGG CTGCAATGCG
251 CCAAGATCCC GCCACTGCAC TCCAGCCTGG GCGACAGAGT GAGACTCCGT
301 CTCCGGGAGC CCACGGCATT GAGCAAACCT CGGCATTATT TGCAGCAAGA
351 GCCTCTGGCA TCCAAATAGC AACCAACACC ACGCCTCTGT AGTGTGCTGC
401 GCAGCCTCA CACTCGAGTC TGAGGCTCCC TGTTTGAGTC CCGCCCTATG
451 CCCAGCTGAG GTTATAGCAC GCTCACCTCC AGAAGAGGTA ACCCAAGCTC
501 TTTACTCTAC TGGAGATCAC CTCTGTCCCC ACTCTGGGCG CTTCTCCCAG
551 CTGACAGAAA ATACCTCCAG CTGATGTCAG AAAATACAGG GCTGGAGGCT
601 GGCGTACAAA GTCAGTCCCC ACAGGCCTAT GGTGGCCCAT AAGCCACGTC
651 TACCCCTGCT CCTCACCTCC ACACCTAAGT TAAGAAATTG AGGCCGGGCG
701 CAGTGGCTCA CGCCTGTAAT CCCAGCACTT TGGGAGGCTG AGGTGGGCGG
751 ACCGCTGAG GTCAGGAATT TGAGACCAGC TTGGCCAACA TGGCAAAACC
801 CCGTCTCTAC TAAAAATACA AAAAGAAAAA ATAGCCGGGC CTGATGTCGC
851 GCACCTGTAA TCCCAGCTAC TCCGGGAGAC TGAGGCGGGA GTATAGCTTG
901 AACCCTGGGA GCAAAGGTTG CAGTGAGGCG AGATCGCACC ACTGCACTCC
951 AGGCTGGGCG ACAGAGTGAG ACTCTGTCTG AAAAAAAAAA AAAGTGCAGG
1001 TACCCCTCTC CAGCTCTCCC CTCCCTACAC ATCCCTCAAA CCGTCCCGCT
1051 GTAATGCACC CGCCTGTTC CTTGGTAACT TGAAGCTGCT TATAGAATGT
1101 GGAGATGGGG GTAATTGAAA GGTCGGCCCA GGCCACAGAG CCCCTGAGCT
1151 CTGCTACCGG CAACCCAGC TGCACTCCCC ACTCTCTGTC ACCAGGAGCT
1201 GCGGGTGCC TGGGATATCC TGGCAGCTCT GCTCAAAATG ATCTACGACT
1251 TCATGAAATT ATTTGGCTCC TCCTCGGGGC CAGGGTGAGT GTCATGGGTT
1301 AATAAGGCCG GCCCCGCTT CAGGAGCGGT CCACTGGGAG ATGTGTGCTG
1351 CGCAGCCCTC TTGCGAAAGC TCTCCCTG TGGGACATTC TGGGCACAAC
1401 CAACAGGCCG GGGGAAATGA GAGGTGATCC ATACTAAAGG GTCAAAGTCC
1451 CCGCACCAGG CAGAGGCCCC AAAACACCGC AGCGTACATG TGCTGCAAGG
1501 CGAGTACGGG TTGGTAAACA AAATATATT CAGATGAGCT CGGGCCGGGT
1551 GACTTAACAG ATGAGGAAGT GTCTCGGGGC CATCGGCGGA GGCGCAGCCC
1601 AGGGGTCCCC AGCTCCCCGC CTCGCCACCT GGGGACAGCC CACGGCCCGG
1651 GGCTCGGGCG CCGCTGTCTG TCGCGGTGCG CAGCGACTAC GGGAACCTCT
1701 CCGCAGCAGA CCGGGTCCCC GCGGCCCGCT CCCCAGGGG CAAGCAAGCG
1751 ACCACAGGGG ACCGGTCCCG GGGCTGGATG TGGCTCATGT CCGAAGCGCA
1801 CGGAGCCGAG CCGGTGTTGC TCAGGGAGGC TGCCCGCCCC TTCACGCAGA
1851 CCCTGCGGCT CTGCGTGCCC TCAGGGAACA GCAAGGTCCG AGCCGGTGTC
1901 GTCGAGGGGG CGACGGGACG GAGGGAGGAG CCTGAGGGGT CCCGGTCGAG
1951 GGAGGGGAGG AGTGGGCGGG GCGGGGTGG GGGCCGTTCC CGCGCTCTCC
2001 TTCGCCTGCG GGCCGGCACT GCTCACCTCT CGTCCAGGGA CATGACGGGC
2051 ACGCCAGGCG CCGTTGCCAC CCGGGATGGC GAGGCCCCG AGCGCTCCCC
2101 GCCCTGCAGT CCGAGTACG ACCTCACGGG CAAGGTGGGT GGGCCTCTTC
2151 CGTGAGACCC CCGCCCTCCT CGGCGTAGC CCCTTCCTGG CTGCGTCTGG
2201 GTTGGACTCA GCCCTTCCCC CAGGCAGCTG CGTCTCCAG AGGAGGGAGG
2251 GAGAGAGGGT CAGGACACAG CCTCTGGGGC CGTCCCAGC TCTAGGTGTC
2301 TCTGCTGGCT TGGTGGGGGC GGGTCGCGGA AGATCGCAA AACTGAGTGA
2351 TCCCCCGGCC GGCCCCAACT CAGTTCTCTT CTGCCACACT CTGGCAAATA
2401 TGAGCCCCCG GGAGCCCATG CTTCTTGGTG AGGGTTAAGC GCGCAACTCT
2451 CGGGGCTCAG GCTGGGAAGG GCTGGGAGAT GGGGACCGAA CGGAGACTCG
2501 GAGAGGACGT CCCCTGCTGG CAGAGGAACT GCGGTTAATG CCATTTTCCG
2551 AGCTAAGCTC TTAGTTGAGA TCTGACATCC AGGTTTAAGG CCTGATGTCC
2601 CCCAGCTGCT CCCCTCCCAT TCCACCCGCT GGAGGCACTG CCTCCCACCT
2651 TCCTCCCTGC AGTCGGAAGC CGCTCCTCCC AGAAGGATGT TGCCAGCCGG
2701 CCTGCAAGT ACTTGGGAAT TTTTCGAACC TGAGAAAGAT TTCAGTGGTT
2751 GGTCTTTCCG ATCCCGCACT TGAGAGAGCT CCAGGGCTGC TCTCTGGGGC
2801 TTGCTCCCTC TACAGGGGTG TCCTGTATGG AAACAGGTAG GGACAGCAGT
2851 GGAAGTGTCT GTCGCTTCC ATCTGTGTCC TTGGAGTGAG CGGGTACCAG
2901 AAAGTAAAG AACTGCTGAG GGAGCCTAGA GCTTCCACTC TTCCTCTGCA
2951 GGGTTGGGGA TGGAGTGAGG GCTGTCTCTG ATTCCGCTGC ATGGCCTTGA
3001 AGGAGACCTG CCTCTCTCTG GGCTCGGTT TCCTCCCCGA CACCAGGGCT
3051 CACCCTTGCT GGGAGCCTCA GCCTCCACCC CAGTGTTCG GGGGAAGCCA

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FIGURE 3A



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3101	CCCTGCAAGT	CATCCGCCCA	GAGCCGTTGA	GATAGGCGTC	CTGTGTGGGC
3151	TTGTGGCAGG	AAATGGGCCC	CTGCACCTC	GGAGAGGAGG	AGCTGTGTGT
3201	GGCCAGGCCC	CAGGCTGAGG	GGGACTGCCT	GACCTTGTGT	CCCTGCAAAC
3251	CAGCTGGGTT	GTTTGCCTAG	GAGGTGGCCA	GGCTAGGCAG	CTGTTTGTGT
3301	TTGGTGGAAT	CACCGAGCTG	GGTGGGTAGC	TGGCATCGTT	TGCTCAAGGC
3351	AGCTGTGATC	TGTAAAGTAC	ACAAAGACTG	GCCCTCCCTC	CCTCCTTCCT
3401	GCTCCAGGGC	TGGGACCCAG	GAGCCAGGGA	GGAGTGCAGG	CTCCAGAAAG
3451	CTCCTATGCC	CCACCCCTTC	ATCTGTTCCC	TGGCCAAGCG	GCATTGGCCG
3501	GAGAGTTGGT	CCCCAGCCTC	CCCGGGCCTG	CCCCAGGGGA	GTGAGTCCAG
3551	GACCCTCTGA	GAAAGCCTGG	CAGGAGCTCC	TTGGACCAGA	CTAGGGGTGA
3601	TGTGGCCAC	AGGCAGACAG	TTCCCACCCT	GGGCCACTCT	TCCCTGGGTC
3651	TTAGGTGATT	CACCACGATG	ATGGGCCCTA	GCCATTAACA	GACTCTAGAA
3701	ATACCTCAAA	GACATTATCC	CTCCTCCTTC	TACCCACTAT	GGAAACCATG
3751	CCACAGAAAG	GTTAAGGAAT	CTTCCTAAAG	TCACACAGTA	GGCCATTTAC
3801	AAATCAAGAC	CATCCTTCA	TACCCCTTCT	GCTCAGCCAC	CCCTGCCTCT
3851	CCACCAGAGT	TAATAATGC	CAGTACCCCA	TGCCCACAAC	AGGAATGCCT
3901	TTGGGCTCCA	CTGTCAATTT	CAGAGCCTCA	AAAATAATTC	AAACCTAGTC
3951	CCTGCTTAAC	CCATTAGGCC	ACCTAACCAG	CAGCTGGGAA	ATTCCAGCAT
4001	TGGATCTAGA	CCCCTGTTAT	CCAAGATTGG	AGAACAGTGG	GACAAAGTGC
4051	TCCTCTCCAC	CATTCTGCG	TGTCCTTGGG	GAAGATGAGC	AGAGCAGAGC
4101	CAGACAGTAA	AGGAGAGGGC	CAGGCCCCCT	CCACAGGTTA	CTCTCTGGT
4151	ACTCCTGCCC	CAGTACCCA	CAGCAACCCC	GGGATGCCGA	TCTGCAGCCA
4201	CATGTCCCAT	GTGGGAGGTT	TCTGCTGAAA	GAACCTCCAA	CTACACATCT
4251	CCCCACTTCA	GTATAAATTT	CAACCTTCCC	TAATTCATGC	AACCTTTTTT
4301	TTTTTTTTTT	TTTTTTGAGA	CAGAGTGTG	CTCTGTCAAC	GAGGCTGGAG
4351	TTCACTGATG	CAATCTCGGC	TCACCTGCAAC	CTCTACCTCC	TGGGTTCAAG
4401	CTATTCTCCT	GTCTCCGCCT	CCCAAGTAAC	TGGGACTACA	GGCGTGTGCC
4451	ACCACCTCCT	GCTAGTTTTT	TGTATTTTTA	GTAGAGATGG	GGTTTCACCT
4501	TGTTGGTCTG	GCTGGTCTCA	AACTCCCAAC	TCAGGTGATC	CGTCCACTTG
4551	GGCACCCAAA	ATGNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
4601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
4651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
4701	NNNNNNNNNN	NNNNNNNNNN	TTCAAGTACC	AGCCTGGCCA	ACATGGTAGA
4751	AACCCCGTCT	CTACTAAAAA	TAAAAAATTA	GCCAGGCGAG	GTGGTGCATG
4801	CCTATAATCC	CAGTACTACA	GGTAGGCTGA	GGCAGGAGAA	TCATTTAAAC
4851	CTGGGAGGTG	GAGGTTGTGG	TGAGCCAAGA	TCTCGCCATT	GCACTCCAGC
4901	CTGGGCAACA	AGAGCAAAAC	TCCGTCTCAA	AAAAAAAAG	AAAGAAAGAA
4951	AGAAAGAAAC	TTCCAAATAA	ATGTTGTGAC	ACAAAAAAA	AAACCCAAAC
5001	AATATTCAAT	ATAGAGTATG	CAAATGACCA	TGCCCCACCC	CCAGCAGATT
5051	CTGATAGACT	CCCTTGGGTG	GGAATCCTTG	TCCAATATAT	TGACACTTCC
5101	CTTCTCTGTC	AGTATAGCCC	AGCCCATGCG	TGTACTCAGC	AGCGGACGAT
5151	GGATGACACA	AGTACACAGA	GGGACGGAAT	CCCTGCATGG	TGTGGCTATG
5201	GGCAAATGTG	GCCACTGTCT	AGATTGTGCA	AATGTGGTGG	TTCTCTGGGG
5251	CCACAGAGCA	CACTTGGGGA	CCTGTTTCATG	GTGAGGTCTC	AACTCCGGCC
5301	TCTAGGAAGT	TGAATGAGGA	CAGGAGGGTC	AGAGGGAGAG	CCTAGGAGGC
5351	TGAGCCAAGG	AGCGTGGAGA	GGAGAGACAG	GGTGAAGGTG	GCGGCTGGCT
5401	TTCTGGAAGC	AGGTGGCCTT	TGGTGGCGTC	AGCATTCGTG	CCAGCCCCCT
5451	CTTCTCTGAT	CCTCTCCATG	TGTCTCTCTC	CTGGAATCCC	AGAAGCTGCC
5501	CCTGACTCCC	CATTAAGTGC	CTCTGCCCCC	ACCCCTAGG	TGATGCTTCT
5551	GGGAGACACA	GGCGTCGGCA	AAACATGTTT	CCTGATCCAA	TTCAAAGACG
5601	GGGCCTTCCT	GTCCGGAACC	TTCATAGCCA	CCGTCGGCAT	AGACTTCAGG
5651	GTGAGGTGGC	TGCAGGCACT	TGCTTCCAGC	AGAGAGCCAG	GGCTGTGGCT
5701	CAGGCATGGG	GGGGTTGCCC	CCACCTTGCT	CACCTTGCT	CCCAGGGACT
5751	CCCGAGGCTC	ATGCTGGGAG	GGCACACAAC	CCGCTCCCCC	AAGACCACAG
5801	AGGTGGCCGG	GTCAAAGGAG	ACTGGGCAAG	GTTGGCTCCT	TGCCCAACTA
5851	TAGGATGCAA	AAAAATGAGA	CTGAGTCTTC	GATTCCAGCT	CCATTCTTGG
5901	GGGACTTCTC	CCAAGCAGAG	CAGCCGCAGG	CACGGCATAA	GCTGAATATC
5951	TTGGCCACAC	GAGCCCCTGC	TCATTGCTCT	CCTACCTGGG	CCCCTTTGGA
6001	AAGGCCTCAA	AGGTCAATCA	GTCTTTCTGG	AGTTCCCAGA	AAGCACAGCC
6051	CTGCACTGGG	TTTAAGAGCT	GGGCTTGGGC	CAGGCATGGT	GGCTCTTGCC
6101	TGTATTCCCA	GCACCTTGGG	AGGCCGAAGC	GGTCAGATCA	CAAGGTCAGG
6151	AGTTTGAGAC	CAGCCTGGCC	AACATGGTGA	AACCCCGTCT	CTACTAAAAA

FIGURE 3B



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6201 TACAAAAATT AGCCAGGTGT AGTGGCACGC TCCTGCAGTC CCAGTACTC
6251 GGGAGGCTGA GGCAGGAGAA TCGCTCAAAT CCGGGTGGTG GAGGTTGCAG
6301 TGAGCTGAGA TCGCGCCACT GCACTCCAGC CTGGGCAACA AAGTGAGACT
6351 GCGTCTCAGA AAAAAAAAAA AAAAAAGAGC TGGGCTGGCC ATGTTGGGAG
6401 ACAGCAGCTC ACCAGGGACC CTCCCTCTCA CCTTGACGAC TCCATCTTAC
6451 AAATCTGCAT CAGGGATGCT AGACGCTGCA CACCTGAAGT GTTCAATAGA
6501 GAAAAGGTCT CACCCTGGCA GGTGGGGCTC TACAGCTTCA AGCAGGCAGA
6551 AAGCGAACAC TTCCTTCACT AGAGAATTAG TGGGCAGCTA AAGAAAAGGT
6601 GCTGTGTCAG ATGTAGCCTC AGGTCCCCAG GATGCAGCA AACACCCCAT
6651 CTCCAGGGGC TCGGTCACAG TCCCAAGGCT AGGCTCCAGG AGAGGGAGAC
6701 CGAAGTGGGG AAAGGGCAGG GCCTCCAGCA GCAACCAGCC CTCCAGCCCT
6751 GGGCTGCCTG ATCCCTGGAG AGAGCCAGGA TGTTTCTCAG GCTCCTCTTG
6801 CCCTGCTGTT GTGAGAAGGC AGTTACAGTC CTCAGAAGGG ACGACTCCAC
6851 AGTGGAGGTG TCTGGGTATG GGGTTCCTGC TGCCCTGATG GTATGATCTG
6901 GCTGGAGACG TCTTGGGGC TCACTGCACC CACTTAGGC CTGGAGAGGG
6951 AACAAGAGAG GACGTCTGCA GAGCTGAGGA GCCACATGAC TCCTGCCTC
7001 CCATCCTCTG CCTTTTTCTC TTTCAGAACA AGGTGGTGAC TGTGGATGGC
7051 GTGAGAGTGA AGCTGCAGGT GAGACCAGAG GCTGGAGTTG GGGAGGGAGG
7101 ATGGAGGACC TGCCCTTCTT TCTCACCTG AACCACAGGA GGCCTGCAGC
7151 CCTGCCCTCC GCCTGGGGCA ATTTCTGTG GGGCCACGG GAGGAAATGG
7201 CTTTTGTTTA TTGACATCT GCAGAAAAG CAGTCCCAG GCACCTCTC
7251 ATCTATGAAC AGCAGCTCCA AATGCCTTCA GACAAGCTTA GCCTCCATCC
7301 ATCTCCTCCC CAGTTGCCAG GGCTTTATCT GCTCTTAGGA GATTGGACAT
7351 CCCCACCCCC TGAGCTAGGG GAGAGGAGAA GATTCTTTTT TTTTCTTTTC
7401 TTTTCTTTTT TTTTTTGAGA TGGAGTCTCG CTCTGTGCCC CAGGCTGGAG
7451 TGCAGTGGCA CAATCTCGGC TCACTGCAAC CTCTGCCTCC CAGGTTTAAG
7501 AGATTCTCCT GCCTCAGCCT CCTGAGTAGC TGAGACTACA GGTGCATGCC
7551 ACCACCTGAG GCTAATTTTT TGTATTTTTA GTAGAGACGG GGTTCCTACTG
7601 TGTTAGCCAG GATGGTCTGG ATCTCCTGAC CTCGTGATCC GCCTGCCTCG
7651 GCCTCCCAAA GTGCTGGGAT TACAGGTGTA AGCCACCGCG CTCGGCTGAG
7701 GAGATGATTT TGAACGAGCT TGAGAAATCA GTAAGTCTA CTGTCCAGGT
7751 CATTGGATGC TCAGGGGCTC ATGAGAACTT AAAGAAGAAA ACAGCCCCAC
7801 CTTCCACAG ATATCTCATA CAACAAAGCA GGCCTGCTCC ACCCAGCACA
7851 TTCCTTGAC CTGCCCTCTT CTGACCATT CTCCATCCCA TCCCTTCCCA
7901 GATCTGGGAC ACCGCTGGGC AGGAACGGTT CCGAAGCGTC ACCCATGCTT
7951 ATTACAGAGA TGCTCAGGGT GAGTCCCTCG CACCCTCCAA CCCCTACCCC
8001 AGCCCCCTGG TAGCATCCGT GCTGCTGCCT AAGTCCCCTC TGTGATCCTC
8051 TCCCTCCAG CTTGCTTCT GCTGTATGAC ATCACCACA AATCTTCTTT
8101 CGACAACATC AGGGTAGGTC CTCCCTTCCC CTGACTCCCA CCCATAAGCA
8151 GCCAAGGCAA GGTCTATGCA GGCTGGGGTT GCTTCTGCCC CTGTGGAAAG
8201 CGGGTGGAGC GTGGAGTCCT CCTGCCCTCT GAAAAACACC TACTTGTGAC
8251 TCAGAAGTCA TATCTGTGCT TTTGTATTG GTGGCCATGT GGGCATGAAG
8301 GCCAAGCAGG CTGTTGTGAC CCTGTGCCAC CTGCATAGCC CTCACTGTGA
8351 TTCACGAGTG TGTTCGTGA CAAAGTGTTC AGAACAGCCC CCACTCCACC
8401 CTGGATAATT ATCCACAGAG ACCAAGGGAA AAACACAACC AGAAAAGTCC
8451 ACACATACAT CCAGGGCAAG TTGCAAGAAA GTGACTCAGT CAGACAGAGT
8501 GAGTGGTTGT ATCCTCACAA CCAACTATT ATAGAGACAA AAATTTGATA
8551 AATTCAAGCA CCAATTTGT TCACGACATT GTATAGGTTT CATGAATCCC
8601 CTGACCTCAA GGACAGTTTG CTGATAAGCA AACTAGGAGA ATAAAACGTT
8651 TATATAGAAA GAGGAAAATC CATGGCACTC ATACTCCTAC CTCCAACCCC
8701 ATGCTCATGG CAGACATCAC TAATCAATCA CAGTACTTTT GATCACTGAA
8751 ACCCTTATGT GGTCTTAGAA TCTTTAACAG GACACTCCAA GAAATCACTG
8801 CTGACAGCCA ACTGATTTGT GAGATAAGGT CTCCATGCAT CTGGATCTTC
8851 CATAGAACTG ATAGTTGCAC AGCATAAAAT GGTGAGGGTG GGGCCATTGT
8901 GGGTTGAGCC ACCAAGGAAG GCCATCCAGG CCTGGATGGG CCAGAACAAA
8951 GGTACAGATG AGAGAACGCA CAGGGTATCG TGTTCAAGGT AGTGAGTAAC
9001 TGAGGATAGT CAAACGGAGC AGAAGAAGAA AGGGGCAGCA GGAGGAAGAG
9051 AATGCCAGTC TCGCACGCCC TCTCCACAG GCCTGGCTCA CTGAGATTCA
9101 TGAGTATGCC CAGAGGGACG TGGTGATCAT GCTGTAGGC AACAGGTGA
9151 GTGGTCCCGG GGCAGGGTCA GCCCAGCCCT GCACTTCCTC AGCCCTAGCC
9201 GGCCCCATAA CCACCAAGA ACAGTTATCT AGGCATCCTT CTGAAAAGG
9251 ACTCTGCAGC CTCCAGCTCA GGGGTACAGC ATATCTGGAG GCTTCTGCCC

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FIGURE 3C



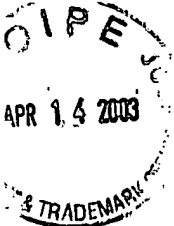
Docket No.: CL001187
Serial No.: 09/817,199
Inventors: SHAO, Wei et al.

Title: ISOLATED HUMAN RAS-LIKE PROTEINS...

9301 ATCCCATCTG CCCCTTCCAG GGAAAGTCCA AGTTGTTGCC TGAGAAATCA
9351 AGGGGTGCCC AGTTCTCAGC CCCCATTAGA GCAGAGTGAA CAGGGTCCCA
9401 GGTCAGGGGC TAAGAGTGCA AAGGGTTAGC CCCAAGTCTG GTCCTATTCC
9451 AAGACCCCTT ACCAAAGGTG AGATCCCAGA GCTGGGAGCT AACTGGGCA
9501 GAAACCCTGG CCCAGGCCA ATCACACCTG CCTGCAGTCC CTTGGGCCAC
9551 CAGCAGAGGG CAGGCAACGC CTGCTTCTGG GGCAAAATAT GGGCCCGCTG
9601 GGGCGGAGGC CTCCTTCCCC AGAGTGACCC ATTTGGGCTT GACAGGCGGA
9651 TATGAGCAGC GAAAGAGTGA TCCGTTCCGA AGACGGAGAG ACCTTGGCCA
9701 GGGTAAGTGA TTGTCTGTGG GACAGGGTGA AGGGTGGGGG CAACCCGACG
9751 CTGGCCCTGA GGACACTCTC TCCCGGGCAG GAGTACGGTG TTCCCTTCCT
9801 GGAGACCAGC GCCAAGACTG GCATGAATGT GGAGTTAGCC TTTCTGGCCA
9851 TCGCCAAGTG AGAGCTGGGC AGGGAAGGGA AGTGTGCGGG GCAGGGCGGC
9901 ACACTCCAGG AATCCAGTAG GGCCCGGCCC CTGGCCAGC CCCTGGACAC
9951 ACCTGCATTC TGCAGGCTGA GGTCCATTG CTCTGGGAGC ACTGGGCCAC
10001 TGGGAGAGGG GAGGGGGCGG CTCAGCTCCT CACCCAGCC CAGCCAGCC
10051 CAGCCAGCC ATGTGTCTCT TCTTCAAGGG AACTGAAATA CCGGGCCGGG
10101 CATCAGGCGG ATGAGCCCAG CTTCCAGATC CGAGACTATG TAGAGTCCCA
10151 GAAGAAGCGC TCCAGCTGCT GCTCCTTCAT GTGAATCCCA GGGGGCAGAG
10201 AGGAGGCTCT GGAGGCACAC AGGATGCAGC CTTCCCCCTC CCAGGCCTGG
10251 CTTATTCCAA GAGGCTGAGC CAATGGGGAG AAAGATGGAG GACTCACTGC
10301 ACAGCCGCTT CCTAGCAGGG AGCTATACTC CAACTCCTAC TTGAGTTCCT
10351 GCGGTCTCCC GCATCCACA GGGAGGGTAA AACACTTAGC TTTTATTTTA
10401 ATAGTACATA ATTTAATACC AAAAAAGGCG CCTGGATCCC CAAAAACCG
10451 AGGCTGGGAG CTAGTGGCCC TTTTGCTTTC TAGGACTTGG GGGGCCGGCC
10501 CTCCCTCCTA AGCATAACAA AGGTGGTGTG GCTCCAGCTC AGCCCAAGGG
10551 GACACAGATG CACTTTGGGG GTGAGGGCAG GTAATGATC CATCGACCC
10601 TCAGTTCAGC TGGACAGAGG CTCAGGTGAC CCCAGCCTTC ACTGTCTCCC
10651 GCTCTCCAGG AGCTTATCTT CGCCCCATCT CCCAAATAAG TGGGCCCTTG
10701 TGCTGTGAGG AAGACCAAG CCTCAGGGAA GATAAGAGAT ATGGAGATGG
10751 GAGGGGGAGG ACAAGGGGCA GAGAGTAGGG TCTAGCTGGC TATCTCTGGC
10801 CTTACTAACA CCCCCCTGGA GGCATGCCCC TTTTCTCCAG CACACAAGCA
10851 CATTGGGGCA CCTGGAATA TTGGTTCCAG GCTCCTGTTC TCTGGACTTC
10901 AGATCCTGGG GGAGCCCCCTC CCCCCCTGA ATCCCTGGCT TAGTACCTT
10951 CCTGCCTGTG CACCTAAAAA CCTCAGGTCA GAACTAGGAA AAGAGTTTGT
11001 TTTTATTTT TTTGAAATGG AGTCTCGTTC TGTCGCCAG GCTGAGGTGC
11051 AGTAGTGCAA TCTCCGCTCA CTACAACCTC CACTCCCTGG GGCTCAAGCG
11101 ATCCTCCAC CTCAGCCGCC GAAGTAGCTG GGACTATAGG TGTGTACCAT
11151 CACACCTGGC TAATTTTTGT ATTTTTTGTG GACACAGGGT TTCGCCATGT
11201 TGCCCAGGCT GGTCTTGAAT TCCTGAGCTC AAGCAACCTG CCGGCCTCGG
11251 CCTCCCAAAG TACTGGGATT ACACGCAGAA GGCACCATGC CCAGGCTAGA
11301 TGTGCTTAT CCAATCCTT TGGCAGGCAT GCAGCTCCAC AGGCGATTTC
11351 TTCAAGCAGC TGAAGTGTTT AGCCCTCCTG GGTTAAGAGC CAGATAAGGA
11401 GAAATCCCTT TCCTAGGTTT GGAATGTGTT GTGAAAAAAA AGAGAAATCC
11451 CTGGCTCCTG GAGCTGGTGG GAGACAAGAT TAAGCAAACC TCCCCTGACA
11501 TGTATCCCTT TGACCCCAAG CTCTGCCTCC TCCCTGACCA CCCATGCCCT
11551 TTCCTTTAAC TTCTCAAACA GATACCAGGG CCTAAACTGC TTTACCTCCC
11601 CTCCTACTGA GTCAGGTTAG GTGGTGGGAG GTCACCCATT TCCGAGTTAA
11651 ACCAATGCAA TATGAGTAAA ACAAGTCAT GTGGGTATGT CTGGGGTAGA
11701 GAGAGGGGTA GCAAGTTCAT GTGTCTCCTT TGGTCACATA TCTCCCAAAG
11751 CTCTGATCCC TGCCATGGGA AGTGGACAGG AAACATGAGG TCATGACCTG
11801 CAGGCATCTT TACTGCAGCT CTGCCGGCCT GGAGGGGGAG AGGGGGAGGA
11851 AGAAGTATGC GCTGCACATT TCTGAGGCTA CTGCATTTGC TTTCAAGGCA
11901 GAAATCTTGC TCTGAGCAGT CAGCGGCTCC AGTTTGGGCC CGATAAGGAA
11951 GTTCTCCGTG GCCTCCCTCA GGCAGAGCAG GGAGGAGGCT GACATTGCCA
12001 GTCTCTTCTG GCGCCCAAGG CAGGTTGCAG GAGATCCAAT CCCATAGACA
12051 GCTCTGGGCC TCTTGCAATT GAGTTTTTCA GAATTAAACT GCAGTATTTT
12101 GGAAAGCACA TCCTGTCCAC TGTTTCTTTG AAGTGAGTGG GGGGGGGGGG
12151 TCTTGTTGAA GGAATTGTCA TTTACTGCCA AAATCATTCC ATCCTCCTTC
12201 CTCAGTGTCT GTCCTCAGAT GGTGAGCTCC CCGCTCAACA GACTGTCTCC
12251 CGCCTCTGTG ACCAGCCTCT CTTTGGCAAG AGGGAGCTAG AAGGCTTTAC
12301 AGTCCTAATC ATTTTCTGTG TGGAAAAAAA AAAAAAAAC CAAGGCTCCT
12351 TTCCCTGTGG CGTGTACCCA GAGGTTGATT ACCTGAGTCT GTCCTGCCTC

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FIGURE 3D



Docket No.: CL001187
Serial No.: 09/817,199
Inventors: SHAO, Wei et al.

Title: ISOLATED HUMAN RAS-LIKE PROTEINS...

```
12401 TCCCCACCCC ACCTCCCTAG CCAAACGCTG CTGCCAAAGC CCACGCTATT
12451 GCCCTAGATG GCCTGTCTTC AGCGGGCTGC CCCTCGAGGT CCCAGGCTCT
12501 CCGCGGAGCC CTCACCTTCC CAGCAGGGAT CAGAACCTGC ACTCCTCTAT
12551 GCGAGTCCTG GGACAGCACA AAGTGGATTA GGGTTAGGGT TCCCACAAAC
12601 GGAAAAATGT TATTCAAACA ACTCTGTAGG GTCCGAGGAG GCCCTCCGTC
12651 TTAATTCTCG AGACTGACCG GCCCTCGCTG CCCCAGACGG GAGCAGTTGC
12701 CCCGGCAACA GCCGCTCCCT CTCAACTGGA GCTGCACCCA GGCTTTGGCT
12751 AAAGGCTGTT AAAACGTTGG CCAGGTGCGG AGGCTCACGT CTGTAATCCC
12801 AGGGCGGATC ACCTGAGGTC AGGAGTTTGA AACCATCTG GCCAACATGG
12851 CGAAATTTTCG TCTCTACTAA AAATACAAAA ATTAGCGGGG CGTGGTGGTG
12901 CGCGCCTGTA ACCCCAGCTG CTCGGGAGGC TGAGGCAGGG GAATCGCTTG
12951 AACC CGGGAG GCGGAGGTTG CAGTGATCCG AGATCGCGCC ACGGCAGTCC
13001 AGCCTGGGCG ACAGAGCGAG ACTCCGTCCTC AAAAAAAAAA AAAAAAGTTA
13051 GGGTCCTTTA CCCGAGGGCC GGCTTTCTCT ACTCCCCGAC ACAGGTAGGG
13101 GAAACCAAGC CGGAGCCGGC GGGCCCACCC GCCCAGAACC GGAATTCCGG
13151 CGAGCCCCGC CCCTGCCACC CCAGCGCCGG CC (SEQ ID NO:3)
```

FEATURES:

Start: 2042
Exon: 2042-2134
Intron: 2135-5539
Exon: 5540-5650
Intron: 5651-7026
Exon: 7027-7068
Intron: 7069-7901
Exon: 7902-7968
Intron: 7969-8060
Exon: 8061-8113
Intron: 8114-9080
Exon: 9081-9146
Intron: 9147-9645
Exon: 9646-9702
Intron: 9703-9780
Exon: 9781-9857
Intron: 9858-10078
Exon: 10079-10181
Stop: 10182

CHROMOSOME MAP POSITION:

Chromosome # 17

ALLELIC VARIANTS (SNPs):

DNA	Position	Major	Minor	Domain
	4259	C	T	Intron
	4325	G	T	Intron
	4348	G	A	Intron
	4924	G	A	Intron
	4983	-	A	Intron
	6710	A	G	Intron
	8624	A	G	Intron
	8661	G	A	Intron
	11754	T	C	Beyond ORF(3')
	11836	A	G	Beyond ORF(3')

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FIGURE 3E



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Context:

DNA
Position
4259

ACCCATTAAGCCACCTAACCAGCAGCTGGGAAATTCAGCATTGGATCTAGACCCCTGTT
ATCCAAGATTGGAGAACAGTGGGACAAAGTGCTCCTCTCCACCATTCTGCGTGTCCCTG
GGGAAGATGAGCAGAGCAGAGCCAGACAGTAAAGGAGAGGGCCACGCCCCCTCCACAGGT
TACCTCCTTGGTACTCCTGCCCGCACTACCCACAGCAACCCCGGATGCCGATCTGCAGC
CACATGTCCCATGTGGGAGGTTTCTGCTGAAAGAACTTCCAACCTACACATCTCCCCACTT
[C, T]
AGTATAAATTTCAACCTTCCCTAATTCATGCAACCTTTTTTTTTTTTTTTTTTTTGGAG
ACAGAGTGTGCTCTGTACCGAGGCTGGAGTTCAGTGATGCAATCTCGGCTCACTGCAA
CCTCTACCTCCTGGGTTCAAGCTATTCTCCTGTCTCCGCTCCCAAGTAACTGGGACTAC
AGGCGTGTGCCACCACTCCTGGCTAGTTTTTTGTATTTTGTAGAGATGGGGTTTCACC
TTGTTGGTCAGGCTGGTCTCAAACCTCCCAACTCAGGTGATCCGTCCACTTGGGCACCCAA (SEQ ID

NO:16)

4325

GATTGGAGAACAGTGGGACAAAGTGCTCCTCTCCACCATTCTGCGTGTCCCTGGGGAAG
ATGAGCAGAGCAGAGCCAGACAGTAAAGGAGAGGGCCACGCCCCCTCCACAGGTTACCTC
CTTGGTACTCCTGCCCGCACTACCCACAGCAACCCCGGGATGCCGATCTGCAGCCACATG
TCCCATGTGGGAGGTTTCTGCTGAAAGAACTTCCAACCTACACATCTCCCCACTTCAGTAT
AAATTTCAACCTTCCCTAATTCATGCAACCTTTTTTTTTTTTTTTTTTTTGAGACAGA
[G, T]
TGTCGCTCTGTACCGAGGCTGGAGTTCAGTGATGCAATCTCGGCTCACTGCAACCTCTA
CCTCCTGGGTTCAAGCTATTCTCCTGTCTCCGCTCCCAAGTAACTGGGACTACAGGCGT
GTGCCACCACTCCTGGCTAGTTTTTTGTATTTTGTAGAGATGGGGTTTCACCTTGTG
GTCAGGCTGGTCTCAAACCTCCCAACTCAGGTGATCCGTCCACTTGGGCACCCAAAATG (SEQ ID

NO:17)

4348

TGCTCCTCTCCACCATTCTGCGTGTCCCTGGGGAAGATGAGCAGAGCAGAGCCAGACAG
TAAAGGAGAGGGCCACGCCCCCTCCACAGGTTACCTCCTTGGTACTCCTGCCCGCACTAC
CCACAGCAACCCCGGATGCCGATCTGCAGCCACATGTCCCATGTGGGAGGTTTCTGCTG
AAAGAACTTCCAACCTACACATCTCCCCACTTCAGTATAAATTTCAACCTTCCCTAATCA
TGCAACCTTTTTTTTTTTTTTTTTTTTTTTTGAGACAGAGTGTGCTCTGTACCGAGGCTG
[G, A]
AGTTCAGTGATGCAATCTCGGCTCACTGCAACCTCTACCTCCTGGGTTCAAGCTATTCTC
CTGTCTCCGCTCCCAAGTAACTGGGACTACAGGCGTGTGCCACCACTCCTGGCTAGTTT
TTTGTATTTTGTAGAGATGGGGTTTCACCTTGTGGTCAGGCTGGTCTCAAACCTCCA
ACTCAGGTGATCCGTCCACTTGGGCACCCAAAATG (SEQ ID NO:18)

4924

TTCAAGTACCAGCCTGGCCAACATGGTAGAAACCCGCTCTACTAAAAATAAAAAATTA
GCCAGGCGAGGTGGTGCATGCCTATAATCCAGCTACTCAGGTAGGCTGAGGCAGGAGAA
TCATTTAAACCTGGGAGGTGGAGTTGTGGTGAGCCAAGATCTCGCCATTGCACTCCAGC
CTGGGCAACAAGAGCAAACTCC
[G, A]
TCTCAAAAAAAAAAAGAAAGAAAGAAAGAAAGAACTTCCAAATAAATGTTGTGACACAA
AAAAAAAAACCCAAACAATATTCAATTATAGAGTATGCAAATGACCATGCCCCACCCAG
CAGATTCTGATAGACTCCCTTGGGTGGGAATCCTTGTCGAATATATTGACACTTCCCTTT
CCTGTGAGTATAGCCAGCCATGCGTGTACTCACGAGCGGACGATGGATGACACAAGTA
CACAGAGGGACGGAATCCCTGCATGGTGTGGCTATGGGCAAATGTGGCCACTGTCTAGAT (SEQ ID

NO:19)

4983

TTCAAGTACCAGCCTGGCCAACATGGTAGAAACCCGCTCTACTAAAAATAAAAAATTA
GCCAGGCGAGGTGGTGCATGCCTATAATCCAGCTACTCAGGTAGGCTGAGGCAGGAGAA
TCATTTAAACCTGGGAGGTGGAGTTGTGGTGAGCCAAGATCTCGCCATTGCACTCCAGC
CTGGGCAACAAGAGCAAACTCCGTCTCAAAAAAAAAAAGAAAGAAAGAAAGAAAGAAAC
TTCCAAATAAATGTTGTGACAC

FIGURE 3F



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[-, A]

AAAAAAAAAACCCAAACAATATTCATTATAGAGTATGCAAATGACCATGCCCCACCCCA
GCAGATTCTGATAGACTCCCTTGGGTGGGAATCCTTGTCCAATATATTGACACTTCCCTT
TCCTGTCAGTATAGCCAGCCCATGCGTGACTCAGAGCGGACGATGGATGACACAAGT
ACACAGAGGGACGGAATCCCTGCATGGTGTGGCTATGGGCAAATGTGCCCACTGTCTAGA
TTGTGCAAATGTGGTGGTTCTCTGGGGCCACAGAGCACACTTGGGGACCTGTTTCATGGTG

(SEQ ID

NO:20)

6710

CACCAGGGACCTCCCTCTCACCTTGACGACTCCATCTTACAAATCTGCATCAGGGATGC
TAGACGCTGCACACCTGAAGTGTTCAATAGAGAAAAGGTCTCACCTGGCAGGTGGGGCT
CTACAGCTTCAAGCAGGCAGAAAGCGAACACTTCCCTTACTAGAGAATTAGTGGGCAGCT
AAAGAAAAGGTGCTGCTGCAGATGTAGCCTCAGGTCCCCAGGATGCAGGCAAACACCCCA
TCTCCAGGGGCTCGGTACAGTCCCAAGGCTAGGCTCCAGGAGAGGGAGACCGAAGTGGG
[A, G]

AAAGGGCAGGGCCTCCAGCAGCAACCAGCCCTCCAGCCCTGGGCTGCCTGATCCCTGGAG
AGAGCCAGGATGTTTCTCAGGCTCCTTGGCCCTGCTGTTGTGAGAAGGCAGTTACAGTC
CTCAGAAGGGACGACTCCACAGTGGAGGTGTCTGGGTATGGGGTTCCTGCTGCCCTGATG
GTATGATCTGGCTGGAGACGGTTCCTGGGGCTCACTGCACCCACTCTAGGCCTGGAGAGGG
AACAGAGAGGACGCTCTGCAGAGCTGAGGAGCCACATGACTCCTGCCTCCCATCCTCTG

(SEQ ID

NO:21)

8624

GTGCCACCTGCATAGCCCTCACTGTGATTACAGAGTGTGTTTCGTGACAAAGTGTTCAGA
ACAGCCCCCACTCCACCCTGGATAATTATCCACAGAGACCAAGGGAAAAACACAACCAGA
AAAGTCCACACATACATCCAGGGCAAGTTGCAAGAAAGTGACTCAGTCAGACAGAGTGAG
TGGTTGTATCCTCACAACCAAACCTATATAGAGACAAAAATTTGATAAATTCAAGCACCA
ATTTTGTTCACGACATTGTATAGGTTTCATGAATCCCTGACCTCAAGGACAGTTTGCTG
[A, G]

TAAGCAAACCTAGGAGAATAAAACGTTTATATAGAAAGAGGAAAAATCCATGGCACTCATA
TCCTACCTCCAACCCCATGCTCATGGCAGACATCACTAATCAATCACAGTACTTTTGATC
ACTGAAACCCCTTATGTGGTCTTAGAATCTTTAACAGGACACTCCAAGAAATCACTGCTGA
CAGCCAACTGATTTGTGAGATAAGGTCTCCATGCATCTGGATCTTCCATAGAAGTATAG
TTGCACAGCATAAAATGGTGAGGGTGGGGCCATTGTGGGTTGAGCCACCAAGGAAGGCCA

(SEQ ID

NO:22)

8661

TGTTTCGTGACAAAGTGTTTCAAGAACGCCCCCACTCCACCCTGGATAATTATCCACAGAG
ACCAAGGGAAAAACACAACCAGAAAAGTCCACACATACATCCAGGGCAAGTTGCAAGAAA
GTGACTCAGTCAGACAGAGTGAGTGGTTGTATCCTCACAACCAAACCTATTATAGAGACAA
AAATTTGATAAATTCAAGCACCAATTTGTTCACGACATTGTATAGGTTTCATGAATCCC
CTGACCTCAAGGACAGTTTGCTGATAAGCAAACCTAGGAGAATAAAACGTTTATATAGAAA
[G, A]

AGGAAAATCCATGGCACTCATACTCCTACCTCCAACCCCATGCTCATGGCAGACATCACT
AATCAATCACAGTACTTTTGATCACTGAAACCCCTTATGTGGTCTTAGAATCTTTAACAGG
ACACTCCAAGAAATCACTGCTGACAGCCAACTGATTTGTGAGATAAGGTCTCCATGCATC
TGGATCTTCCATAGAAGTATAGTTGCACAGCATAAAATGGTGAGGGTGGGGCCATTGTG
GGTTGAGCCACCAAGGAAGGCCATCCAGGCCTGGATGGGCCAGAACAAAGGTACAGATGA

(SEQ ID

NO:23)

11754

GCTCCTGGAGCTGGTGGGAGACAAGATTAAGCAAACCTCCCCTGACATGTATCCCCTTGA
CCCCAAGCTCTGCCTCCTCCCTGACCACCCATGCCCTTTCCTTTAACTTCTCAAACAGAT
ACCAGGGCCTAAACTGCTTTACCTCCCCTCCTACTGAGTCAGGTAGGTGGTGGGAGGTC
ACCCATTTCCGAGTTAAACCAATGCAATATGAGTAAACAAAGTCATGTGGGTATGTCTG
GGGTAGAGAGAGGGGTAGCAAGTTTATGTGTCTCCTTGGTTCATATCTCCCAAAGCTC
[T, C]

GATCCCTGCCATGGGAAGTGGACAGGAAACATGAGGTGATGACCTGCAGGCATCTTTACT
GCAGCTCTGCCGGCTTGGAGGGGGAGAGGGGGAGGAAGAAGTATGCGCTGCACATTTCTG
AGGCTACTGCATTTGCTTTCAAGGCAGAAATCTTGCTCTGAGCAGTCAGCGGCTCCAGTT
TGGGCCCGATAAGGAAGTTCTCCGTGGCCTCCCTCAGGCAGAGCAGGGAGGAGGCTGACA
TTGCCAGTCTCTTCTGGGGCCCAAGGCAGGTTGCAGGAGATCCAATCCCATAGACAGCTC

(SEQ ID

NO:24)

11836

GACCACCCATGCCCTTTCCTTTAACTTCTCAAACAGATACCAGGGCCTAAACTGCTTTAC
CTCCCCTCCTACTGAGTCAGGTTAGGTGGTGGGAGGTACCCATTTCCGAGTTAAACCAA

FIGURE 3G



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Inventors: SHAO, Wei et al.

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TGCAATATGAGTAAACAAAGTCATGTGGGTATGTCTGGGGTAGAGAGAGGGGTAGCAAG
TTCATGTGTCCTCCTTGGTCACATATCTCCCAAAGCTCTGATCCCTGCCATGGGAAGTGG
ACAGGAAACATGAGGTCATGACCTGCAGGCATCTTTACTGCAGCTCTGCCGGCCTGGAGG
[A, G]
GGAGAGGGGGAGGAAGAAGTATGCGCTGCACATTTCTGAGGCTACTGCATTTGCTTTCAA
GGCAGAAATCTTGCTCTGAGCAGTCAGCGGCTCCAGTTTGGGCCCCGATAAGGAAGTTCTC
CGTGGCCTCCCTCAGGCAGAGCAGGGAGGAGGCTGACATTGCCAGTCTCTTCTGGGGCCC
AAGGCAGGTTGCAGGAGATCCAATCCCATAGACAGCTCTGGGCCTCTTGCATTTGAGTTT
TTCAGAATTAACTGCAGTATTTTGGAAAGCACATCCTGTCCACTGTTTCTTTGAAGTGA

NO: 25)

(SEQ ID

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FIGURE 3H